

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:44:14 ; Search time 39 Seconds
(without alignments)
14,803 Million cell updates/sec

Title: US-10-648-854-10

Perfect score: 32

Sequence: 1 HAVHAV 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	32	100.0	250	2	C84310	precorrin-3 methyl
2	32	100.0	263	2	H95875	probable spermidin
3	32	100.0	649	2	D96025	probable adenylate
4	31	96.9	351	2	AF0975	probable lacI fami
5	31	96.9	418	2	S46315	aspartate transami
6	31	96.9	514	2	S72847	hypothetical prote
7	31	96.9	554	2	C70512	hypothetical prote
8	29	90.6	117	2	B70572	hypothetical prote
9	29	90.6	209	2	H83133	hypothetical prote
10	29	90.6	253	2	AF3625	cell division inhi
11	29	90.6	318	2	S44970	lmbW protein - Str
12	29	90.6	345	2	T37139	hypothetical prote
13	29	90.6	475	2	S38502	ribulose-bisphosph
14	29	90.6	511	2	S3686	monocamine transp
15	29	90.6	511	2	S43685	monocamine transp
16	29	90.6	547	2	G71307	probable oligopept
17	29	90.6	621	2	G31844	tra protein - Stre
18	29	90.6	1774	2	T17421	polyketide synthas
19	28	87.5	164	2	AC3046	hypothetical prote
20	28	87.5	183	2	S29088	ubiquitin-protein
21	28	87.5	214	2	AC3351	proteinnase I (EC 3
22	28	87.5	261	2	T11028	cytochrome-c oxida
23	28	87.5	261	2	T32399	hypothetical prote
24	28	87.5	263	2	AG3211	hypothetical prote
25	28	87.5	265	2	T24600	hypothetical prote
26	28	87.5	281	2	A71354	hypothetical prote
27	28	87.5	310	2	S58090	probable membrane
28	28	87.5	315	2	H83740	hypothetical prote
29	28	87.5	320	1	DAAL2E	catechol 2,3-dioxy

30	28	87.5	321	2	AG3131	dihydrodipicolinat
31	28	87.5	321	2	D98156	probable dihydrodi
32	28	87.5	327	2	S56162	MDCR15 protein - h
33	28	87.5	372	2	S26667	G protein-coupled
34	28	87.5	374	2	S42628	G protein-coupled
35	28	87.5	374	2	S32785	G protein-coupled
36	28	87.5	397	2	T08345	hypothetical prote
37	28	87.5	444	2	E71317	probable hexokinas
38	28	87.5	448	2	B69965	D-serine dehydrata
39	28	87.5	457	2	AG2728	polysaccharide bio
40	28	87.5	480	2	AH2333	cardiolipin syntha
41	28	87.5	522	2	H97509	probable glycosyl
42	28	87.5	556	2	JCS132	alpha-amylase (EC
43	28	87.5	571	2	AG0144	D-lactate dehydrog
44	28	87.5	575	2	JC7727	4-alpha-D-(1-34)-
45	28	87.5	677	2	T02951	probable mitogen a

ALIGNMENTS

RESULT 1

C84310 precorrin-3 methylase [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 12-Jul-2004

C;Accession: C84310

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li;

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: C84310

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-250 <STO>

A;Cross-references: UNIPROT:Q9HPM0; UNIPARC:UPI000006390E; GB:A5004437; NID:GI0581053; P;

C;Genetics:

C;Gene: cbiJ

C;Superfamily: precorrin-6Y methyltransferase CbiE

Query Match 100.0%; Score 32; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAVHAV 6

Db 28 HAVHAV 33

RESULT 2

H95875

probable spermidineputrescine ABC transporter permease protein SMB20282 [imported] - Sin

C;Species: Sinorhizobium meliloti

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: H95875

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-263 <KUR>

A;Cross-references: UNIPROT:Q92W07; UNIPARC:UPI00000CB48B; GB:AL591985; PIDN:CAC48672.1;

A;Experimental source: strain 1021, megaplasmid pSymb

R;Galibert, P.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federepief, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaut, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: *SMB20282*
A:Genome: plasmid
C:Superfamily: spermidine/putrescine transport system permease protein porI

Query Match 100.0%; Score 32; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6
|||||
DB 142 HAVHAV 147

RESULT 3
D96025
probable adenylate cyclase (EC 4.6.1.1) [imported] - *Sinorhizobium meliloti* (strain 1021)
C:Species: *Sinorhizobium meliloti*
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: D96025
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: D96025
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-649 <KUR>
A:Cross-references: UNIPROT:Q92TN9; UNIPARC:UPI00000CB893; GB:AL591985; PIDN:CAC49868.1;
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaut, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: *cyaK*; *SMB20776*
A:Genome: plasmid
C:Keywords: phosphorus-oxygen lyase

Query Match 100.0%; Score 32; DB 2; Length 649;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6
|||||
DB 475 HAVHAV 480

RESULT 4
AF0975
probable lacI family transcription regulator regulator STY4100 [imported] - *Salmonella* e
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A:Note: this species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AF0975
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moulle, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0975
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-351 <PAR>
A:Cross-references: UNIPARC:UPI000005A70F; GB:AL513382; PIDN:CAD03298.1; PID:g16504918;
C:Genetics:
A:Gene: *STY4100*

Query Match 96.9%; Score 31; DB 2; Length 351;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6
|||||
DB 228 HAVHAV 233

RESULT 5
S46315
aspartate transaminase (EC 2.6.1.1) - alfalfa
N:Alternate names: aspartate aminotransferase
C:Species: *Medicago sativa* (alfalfa)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S46315; S18616; S18039
R:Gregerson, R.G.; Miller, S.S.; Petrowski, M.; Gantt, J.S.; Vance, C.P.
Plant Mol. Biol. 25, 387-399, 1994
A:Title: Genomic structure, expression and evolution of the alfalfa aspartate aminotran
A:Reference number: S46315; MUID:94325464; PMID:8049365
A:Accession: S46315
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <GRE>
A:Cross-references: UNIPROT:P28011; UNIPARC:UPI00001250CD; EMBL:L25334; NID:g413725; PI
A:Note: the authors translated the codon TAC for residue 301 as Ile and CAT for residue
R:Juvard, M.K.; Kahn, M.L.
Mol. Gen. Genet. 231, 97-105, 1991
A:Title: Isolation and analysis of a cDNA clone that encodes an alfalfa (*Medicago sativ*
A:Reference number: S18616; MUID:92092970; PMID:1753949
A:Accession: S18616
A:Molecule type: mRNA
A:Residues: 2, RE, 5-407, D, 409-418 <UDV>
A:Cross-references: UNIPARC:UPI000016DS4D; EMBL:X61577; NID:g19570; PIDN:CAA43779.1; PI
A:Experimental source: var. Ladak
C:Genetics:
A:Gene: *aat-1*

A:Introns: 31/3; 55/3; 76/2; 104/2; 137/3; 178/1; 232/3; 278/3; 319/2; 351/1; 391/2
C:Superfamily: aspartate aminotransferase
C:Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate
F:264/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 96.9%; Score 31; DB 2; Length 418;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6
|||||
DB 408 HAVHAV 413

RESULT 6
S72847
hypothetical protein B2126 Cl 172 - *Mycobacterium leprae*
C:Species: *Mycobacterium leprae*
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S72847
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Description: *Mycobacterium leprae* cosmid B2126.
A:Reference number: S72585
A:Accession: S72847
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-514 <SMT>
A:Cross-references: UNIPROT:Q49779; UNIPARC:UPI00000D435D; EMBL:U00017; NID:g466994; PI
C:Superfamily: proteasome complex-related protein

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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:40:44 ; Search time 296 Seconds
(without alignments)
18.750 Million cell updates/sec

Title: US-10-648-854-10

Perfect score: 32

Sequence: 1 HAVHAV 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	132	2	Q2S639_9SPHI
2	32	100.0	133	2	Q2S4V3_9SPHI
3	32	100.0	138	2	Q5U126_DROME
4	32	100.0	193	2	Q2RG99_MOOTH
5	32	100.0	232	2	Q37E89_RHOA
6	32	100.0	233	2	Q8FMS9_COREF
7	32	100.0	250	2	Q9HPM0_HALSA
8	32	100.0	263	2	Q2W071_RHIME
9	32	100.0	282	2	Q3WNS8_RHIZ
10	32	100.0	373	2	Q3WFX8_9ACTO
11	32	100.0	399	2	Q35984_9BRAD
12	32	100.0	407	2	Q3VSH6_DROME
13	32	100.0	540	2	Q58DN1_BOVIN
14	32	100.0	602	2	Q4PGX2_USTMA
15	32	100.0	611	2	Q40Q64_DESAC
16	32	100.0	613	2	Q4A066_PELCD
17	32	100.0	615	1	LMO6_HUMAN
18	32	100.0	615	2	Q53XR5_HUMAN
19	32	100.0	615	2	Q6IAE4_HUMAN
20	32	100.0	636	2	Q3JRS7_BURPL
21	32	100.0	649	2	Q32TN9_RHIME
22	32	100.0	719	2	Q37FV8_RHOA
23	32	100.0	811	2	Q5NLT4_ZYMMO
24	32	100.0	1327	2	Q6C4J5_YARLI
25	32	100.0	1608	2	Q4HY99_GIBZE
26	31	96.9	161	2	Q39ZB2_GEOMG
27	31	96.9	163	2	Q746T5_GEOMG
28	31	96.9	206	2	Q8GN13_BRAJA
29	31	96.9	222	2	Q89G54_BRAJA
30	31	96.9	245	2	Q60424_METCA
31	31	96.9	252	2	Q445V4_SOLUS

32 31 96.9 257 2 Q5W2P3_LEGPL
33 31 96.9 257 2 Q5X891_LEGPA
34 31 96.9 267 2 Q8Z478_PYRAE
35 31 96.9 282 2 Q5ZY55_LEGPH
36 31 96.9 289 2 Q704A1_THERE
37 31 96.9 290 2 Q7U9U4_SYNPX
38 31 96.9 292 2 Q6SGW1_9BACT
39 31 96.9 292 2 Q8KZ78_9PROT
40 31 96.9 306 2 Q3ANAL_SYNSC
41 31 96.9 318 2 Q38FI6_9TRYP
42 31 96.9 323 2 Q5PNQ1_BRARE
43 31 96.9 323 2 Q5XJ72_BRACHYDANIO
44 31 96.9 334 2 Q8ZL59_SALTY
45 31 96.9 349 2 Q37AS5_RHOA

Q5W2P3 legionella
Q5X891 legionella
Q8Z478 pyrobaculum
Q5ZY55 legionella
Q704A1 thermoprote
Q7U9U4 synchococc
Q6SGW1 uncultured
Q8KZ78 uncultured
Q3ANAL synchococc
Q38FI6 trypanosoma
Q5PNQ1 brachydanio
Q5XJ72 brachydanio
Q8ZL59 salmonella
Q37AS5 rhodopsuendo

ALIGNMENTS

RESULT 1

Q2S639_9SPHI PRELIMINARY; PRT; 132 AA.
AC Q2S639;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE IS605 family transposase orfa.
GN ORFNames=SRU_0191;
OS Salinibacter ruber DSM 13855.
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
OC Crenotrichaceae; Salinibacter.
OX NCBI_TaxID=309807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 13855;
RX PubMed=16330755; DOI=10.1073/pnas.0509073102;
RA Mongodin E.P., Nelson K.E., Daugherty S., Deboy R.T., Wister J.,
Khouri A., Weidman J., Walsh D.A., Papke R.T., Sanchez Perez G.,
Sharma A.K., Nesbo C.L., Macleod D., Bapteste E., Doolittle W.F.,
Charlebois R.L., Legault B., Rodriguez-Valera F.,
RT "The genome of Salinibacter ruber: Convergence and gene exchange among
hyperhalophilic bacteria and archaea.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:18147-18152(2005).
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CC Distributed under the Creative Commons Attribution-NoDerivs License
DR EMBL; CP000159; ABC44598.1; -; Genomic DNA.
SQ SEQUENCE 132 AA; 15486 MW; 64801367876A794 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6
|||
DB 13 HAVHAV 18

RESULT 2

Q2S4V3_9SPHI PRELIMINARY; PRT; 133 AA.
AC Q2S4V3;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE IS605 family transposase orfa.
GN ORFNames=SRU_0640;
OS Salinibacter ruber DSM 13855.
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
OC Crenotrichaceae; Salinibacter.
OX NCBI_TaxID=309807;
RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DSM 13855;
 RX PubMed=16330755; DOI=10.1073/pnas.0509073102;
 RA Mongodin E.F., Nelson K.S., Daugherty S., Deboy R.T., Wister J.,
 RA Khouri H., Weidman J., Walsh D.A., Papke R.T., Sanchez Perez G.,
 RA Sharma A.K., Nesbo C.L., Macleod D., Baptiste E., Doolittle W.F.,
 RA Charlebois R.L., Legault B., Rodriguez-Valera F.;
 RT "The genome of *Salinibacter ruber*: Convergence and gene exchange among
 RT hyperhalophilic bacteria and archaea";
 RL Proc. Natl. Acad. Sci. U.S.A. 102:18147-18152(2005).
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 CC -----
 DR EMBL: CP000159; ABC44828.1; --; Genomic DNA
 SQ SEQUENCE 133 AA; 15851 MW; 923FBE6B892A8CAC CRC64;
 Query Match 100.0%; Score 32; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 70; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0;
 QY 1 HAVHAV 6
 DB 14 HAVHAV 19
 RESULT 3
 QSUI126_DROME
 ID QSUI126_DROME PRELIMINARY; PRT; 138 AA.
 AC QSUI126;
 DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE LPI2967P.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkley;
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: BT016056; AA326951.1; --; mRNA.
 DR GO:0042302; F:structural constituent of cuticle; IEA.
 DR InterPro: IPR00618; Insect_cuticle.
 DR Pfam: PF00379; Chitin_bind_4; 1.
 DR PRINTS: PR00947; CUTICLE.
 DR PROSITE: PS00233; CUTICLE; 1.
 SQ SEQUENCE 138 AA; 14892 MW; 0E2D1525EB301A71 CRC64;
 Query Match 100.0%; Score 32; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HAVHAV 6
 DB 37 HAVHAV 42
 RESULT 4
 Q2RGQ9_MOOTH
 ID Q2RGQ9_MOOTH PRELIMINARY; PRT; 193 AA.
 AC Q2RGQ9;
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-FEB-2006, entry version 2.

DE Peptidase C56, PfPI.
 GN ORFNames=MoTh_2087;
 OS Moorella thermoacetica ATCC 39073.
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 OC Thermoanaerobacteriaceae; Moorella group; Moorella.
 OX NCBI_TaxID=264732;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 39073;
 RG US DOE Joint Genome Institute;
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pittluck S., Chertkov O., Saunders E.H.,
 RA Bretin T., Bruce D., Han C., Tapia R., Gilna P., Schmutz J.,
 RA Larimer F., Land M., Kyrpides N., Anderson I., Richardson P.,
 RA Ragsdale S.;
 RT "Complete sequence of *Moorella thermoacetica* ATCC 39073";
 RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: CP000232; ABC20380.1; --; Genomic DNA
 SQ SEQUENCE 193 AA; 20743 MW; 63BF797A36848ED6 CRC64;
 Query Match 100.0%; Score 32; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HAVHAV 6
 DB 31 HAVHAV 36
 RESULT 5
 Q37EE9_RHOA
 ID Q37EE9_RHOA PRELIMINARY; PRT; 232 AA.
 AC Q37EE9;
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Hypothetical protein.
 GN ORFNames=RPDDRAFT_0342;
 OS Rhodopseudomonas palustris B125.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=316057;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B125;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pittluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of *Rhodopseudomonas*
 RT palustris B125";
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B125;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome of *Rhodopseudomonas palustris* B125";
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL: AAK201000013; EA084143.1; --; Genomic DNA
 KW Hypothetical protein.
 SQ SEQUENCE 232 AA; 24151 MW; F26428058EB16451 CRC64;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:40:25 ; Search time 200 Seconds
(without alignments)
13.716 Million cell updates/sec

Title: US-10-648-854-10

Perfect score: 32

Sequence: 1 HAVHAV 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*
- 10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	6	2 AAY09097	Aay09097 A represe
2	32	100.0	269	8 ADX67048	Adx67048 Plant ful
3	32	100.0	401	8 ADT60801	Adt60801 Plant pol
4	32	100.0	410	4 ABB62935	Abb62935 Drosophil
5	32	100.0	566	7 ABO69053	Abc69053 Pseudomon
6	32	100.0	615	4 AAM79239	Aam79239 Human pro
7	32	100.0	615	7 ADJ69107	Adj69107 Human hea
8	32	100.0	645	4 AAM80223	Aam80223 Human pro
9	32	100.0	1422	2 AAR82066	Aar82066 Hepatitis
10	32	100.0	1422	3 AAB09036	Aab09036 Hepatitis
11	31	96.9	132	2 AAR28990	Aar28990 Encoded b
12	31	96.9	136	6 ABP99306	Abp99306 Orthosomy
13	31	96.9	215	2 AAR28989	Aar28989 Encoded b
14	31	96.9	257	9 AEB36998	Aeb36998 L. pneumo
15	31	96.9	283	9 AEB36280	Aeb36280 L. pneumo
16	31	96.9	487	8 ADT60381	Adt60381 Plant pol
17	31	96.9	487	8 ADT60382	Adt60382 Plant pol
18	30	93.8	488	8 ADT60384	Adt60384 Plant pol
19	29	90.6	199	7 ADF38938	Adf38938 Corynebac
20	29	90.6	252	7 ABO78691	Abc78691 Pseudomon
21	29	90.6	268	4 AAM48176	Aam48176 Thermus t
22	29	90.6	268	8 ADJ67926	Adj67926 T. thermo
23	29	90.6	268	8 ADJ68138	Adj68138 T. thermo

24	29	90.6	268	8	ADK01216	DNA polym
25	29	90.6	268	8	ADJ79435	T. thermo
26	29	90.6	268	8	ADJ84875	T. thermo
27	29	90.6	268	8	ADM77663	DNA polym
28	29	90.6	268	8	ADM66330	T. thermo
29	29	90.6	268	8	ADO04383	T. thermo
30	29	90.6	268	8	ADP82460	Thermus t
31	29	90.6	268	8	ADP82460	Thermus t
32	29	90.6	268	9	ADY55158	T. thermo
33	29	90.6	268	9	ADZ76734	T. thermo
34	29	90.6	268	9	AEA24742	Thermus t
35	29	90.6	268	9	AEA34165	Thermus t
36	29	90.6	268	9	AEBS1569	DNA polym
37	29	90.6	350	8	ADY07855	Plant ful
38	29	90.6	442	6	ABU34984	Protein e
39	29	90.6	447	8	ADL05393	M. catarr
40	29	90.6	676	7	ADM25638	Hyperther
41	29	90.6	917	6	ABU19998	Protein e
42	29	90.6	1051	7	ABO70399	Pseudomon
43	28	87.5	11	4	AAM99278	Vaccine r
44	28	87.5	15	7	ADM33896	HLA bindi
45	28	87.5	15	7	ADM35129	HLA bindi

ALIGNMENTS

RESULT 1

RAY09097
ID AAY09097 standard; peptide; 6 AA.

XX AC AAY09097;

XX DT 07-JUL-1999 (first entry)

XX DE A representative HAV sequence of a cell adhesion modulating agent.

XX KW Cadherin; modulating agent; cadherin-mediated cell adhesion; cancer;
drug delivery; bladder tumour; ovarian tumour; melanoma; cell adhesion;
wound healing; neurite outgrowth; demyelinating neurological disease;
multiple sclerosis; carcinoma; leukemia; melanoma; angiogenesis;
apoptosis; diabetes; rheumatoid arthritis; immune system; pregnancy;
vasopermeability; spinal cord injury; synaptic stability.

XX OS Synthetic.

XX PN WO9916791-A2.

XX PD 08-APR-1999.

XX PF 29-SEP-1998; 98WO-CA000902.

XX PR 29-SEP-1997; 97US-00939853.

XX PA (ADHE-) ADHEREX INC.

XX PI Blaschuck OW, Gour BJ;

XX DR WPI; 1999-263686/22.

XX PT Modulating cadherin-mediated cell adhesion useful for treating

XX PS neurological disease and cancer.

XX PS Disclosure; Page 15; 148pp; English.

XX CC The invention relates to methods using cadherin modulating agents,
particularly peptides containing the sequence HAV or antibodies, for
enhancing or inhibiting cadherin-mediated cell adhesion. The methods can
be used to treat diseases or other conditions characterized by
undesirable cell adhesion or to facilitate drug delivery to a specific
tissue or tumour (such as bladder tumours, ovarian tumours or melanomas).
They can also be used to enhance cell adhesion (e.g. supplement or
replace stitches or to facilitate wound healing). They can also be used

CC for enhancing and/or directing neurite outgrowth. The methods can also be
 CC used for treating demyelinating neurological disease, e.g. multiple
 CC sclerosis. The methods can also be used for e.g. enhancing drug delivery,
 CC treating cancers (such as carcinomas, leukemia or melanomas), inhibiting
 CC angiogenesis, enhancing adhesion of foreign tissue implanted in a mammal,
 CC inducing apoptosis in cadherin-expressing cells, e.g. for treating
 CC diabetes or rheumatoid arthritis, modulating the immune system, for
 CC preventing pregnancy, increasing vasopermeability, treating spinal cord
 CC injuries or inhibiting synaptic stability

XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 32; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6
 |||||
 Db 1 HAVHAV 6

RESULT 2

ADX67048
 ID ADX67048 standard; protein; 269 AA.

XX AC ADX67048;

XX DT 21-APR-2005 (first entry)

XX DE Plant full length insert polypeptide seqid 37891.

XX KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.

XX OS Unidentified.

XX PN US2004034888-A1.

XX PD 19-FEB-2004.

XX PF 28-APR-2003; 2003US-00425114.

XX PR 06-MAY-1999; 99US-00304517.

XX PR 05-NOV-2001; 2001US-00985678.

XX PA (JIUJ//) LIU J.

XX PA (ZHOU//) ZHOU Y.

XX PA (KOVA//) KOVALIC D K.

XX PA (SCRE//) SCREEN S E.

XX PA (TABA//) TABASKA J E.

XX PA (CAOY//) CAO Y.

XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.

XX Claim 1; SEQ ID NO 37891; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX SQ Sequence 269 AA;

Query Match 100.0%; Score 32; DB 8; Length 269;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6

|||||

Db 74 HAVHAV 79

RESULT 3

ADT60801

ID ADT60801 standard; protein; 401 AA.

XX AC ADT60801;

XX DT 13-JAN-2005 (first entry)

XX DE Plant polypeptide, SEQ ID 10878.

XX KW plant; transgenic; cold tolerance; growth rate; drought tolerance;
 KW disease resistance; galactomannan production; plant growth regulator;
 KW heat tolerance; herbicide tolerance; lignin production;
 KW extreme osmotic condition tolerance; pathogens resistance;
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.

XX OS Viridiplantae.

XX PN US2004216190-A1.

XX PD 28-OCT-2004.

XX PF 18-DEC-2003; 2003US-00739930.

XX PR 28-APR-2003; 2003US-00424599.

XX PR 28-APR-2003; 2003US-00425115.

XX PA (KOVA//) KOVALIC D K.

XX PI Kovalic DK;

XX WI; 2004-757369/74.

XX New recombinant DNA constructs useful in the field of biochemistry and
 PT genetics, and in particular for producing transgenic plants with improved
 PT biological characteristics.

XX Claim 2; SEQ ID NO 10878; 14pp; English.

XX The invention relates a recombinant DNA construct comprising a
 CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
 CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
 CC Arabidopsis, wheat and rape but the specification does not indicate which
 CC sequences is derived from which organism. Also included is a method of
 CC producing a plant having an improved property, comprising transforming a
 CC plant with a recombinant DNA construct comprising a promoter region

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 23, 2006, 21:01:15 ; Search time 185 Seconds
(without alignments)
15.023 Million cell updates/sec

Title: US-10-648-854-10
Perfect score: 32
Sequence: 1 HAVHAV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /EMC Celleria_SIDS3/prodata/2/pubpaa/US08_PUBCOMB.psp:
3: /EMC Celleria_SIDS3/prodata/2/pubpaa/US09_PUBCOMB.psp:
4: /EMC Celleria_SIDS3/prodata/2/pubpaa/US10_PUBCOMB.psp:
5: /EMC Celleria_SIDS3/prodata/2/pubpaa/US10_PUBCOMB.psp:
6: /EMC Celleria_SIDS3/prodata/2/pubpaa/US11_PUBCOMB.psp:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	6	3	US-09-778-026-10
2	32	100.0	6	4	US-10-648-854-10
3	32	100.0	74	4	US-10-424-599-219794
4	32	100.0	110	4	US-10-767-701-62121
5	32	100.0	269	4	US-10-425-114-37891
6	32	100.0	335	6	US-11-096-568A-9644
7	32	100.0	401	5	US-10-739-930-10878
8	32	100.0	410	6	US-11-037-143-15597
9	32	100.0	514	4	US-10-437-963-191565
10	32	100.0	615	3	US-09-939-853A-16
11	32	100.0	615	4	US-10-087-887-75
12	32	100.0	615	4	US-10-408-765A-913
13	32	100.0	1422	2	US-08-424-550B-81
14	31	96.9	76	4	US-10-425-115-361107
15	31	96.9	106	4	US-10-425-115-355177
16	31	96.9	136	4	US-10-107-431-199
17	31	96.9	487	5	US-10-739-930-10458
18	31	96.9	487	5	US-10-739-930-10459
19	31	96.9	491	5	US-10-732-923-6255
20	30	93.8	488	5	US-10-739-930-10461
21	29	90.6	57	4	US-10-424-599-231009
22	29	90.6	58	4	US-10-424-599-236417
23	29	90.6	58	6	US-11-188-298-8669
24	29	90.6	67	4	US-10-424-599-174317
25	29	90.6	98	4	US-10-425-115-251082
26	29	90.6	109	4	US-10-767-701-47481
27	29	90.6	132	4	US-10-425-115-242942

28	90.6	172	4	US-10-425-115-203226	Sequence 203226,
29	90.6	199	4	US-10-326-671-50	Sequence 50, Appl
30	90.6	234	6	US-11-096-568A-8949	Sequence 8949, Ap
31	90.6	268	4	US-10-671-403-156	Sequence 156, App
32	90.6	268	4	US-10-671-419-156	Sequence 156, App
33	90.6	268	4	US-10-670-844-156	Sequence 156, App
34	90.6	268	4	US-10-671-134-156	Sequence 156, App
35	90.6	268	4	US-10-673-098-156	Sequence 156, App
36	90.6	268	4	US-10-672-638-156	Sequence 156, App
37	90.6	268	4	US-10-673-127-156	Sequence 156, App
38	90.6	268	4	US-10-670-817-156	Sequence 156, App
39	90.6	268	4	US-10-673-119-156	Sequence 156, App
40	90.6	268	4	US-10-746-167-17	Sequence 17, Appl
41	90.6	268	4	US-10-746-167-94	Sequence 94, Appl
42	90.6	268	4	US-10-671-207-156	Sequence 156, App
43	90.6	268	5	US-10-673-120-156	Sequence 156, App
44	90.6	268	5	US-10-671-413-156	Sequence 156, App
45	90.6	268	5	US-10-671-859-156	Sequence 156, App

ALIGNMENTS

RESULT 1
US-09-778-026-10
; Sequence 10, Application US/09778026
; Publication No. US20030013655A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING
; CELL ADHESION
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; City: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/778,026
; FILING DATE: 05-Feb-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 32,391
; REFERENCE/DOCKET NUMBER: 100086.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-778-026-10

Query Match 100.0%; Score 32; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6
| | | | |
DB 1 HAVHAV 6

RESULT 2

US-10-648-854-10
; Sequence 10, Application US/10648854
; Publication No. US20040132651A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING
; CELL ADHESION
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/648,854
; FILING DATE: 25-Aug-2003
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jeffrey E. Hundley
; REGISTRATION NUMBER: 42,676
; REFERENCE/DOCKET NUMBER: 100086.402C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-648-854-10

Query Match 100.0%; Score 32; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAVHAV 6
Db 1 HAVHAV 6

RESULT 3

US-10-424-599-219794
; Sequence 219794, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219794
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40501C.1.1.pep

US-10-424-599-219794

Query Match 100.0%; Score 32; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HAVHAV 6
Db 27 HAVHAV 32

RESULT 4

US-10-767-701-62121
; Sequence 62121, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 62121
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURES:
; OTHER INFORMATION: Clone ID: 9856360.pep
US-10-767-701-62121

Query Match 100.0%; Score 32; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAVHAV 6
Db 22 HAVHAV 27

RESULT 5

US-10-425-114-37891
; Sequence 37891, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37891
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURES:
; OTHER INFORMATION: Clone ID: LIB3066-028-C4_FLI.pep
US-10-425-114-37891

Query Match 100.0%; Score 32; DB 4; Length 269;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAVHAV 6
Db 1 HAVHAV 6

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 23, 2006, 21:01:40 ; Search time 22 Seconds
(without alignments)
6.231 Million cell updates/sec

Title: US-10-648-854-10

Perfect score: 32

Sequence: 1 HAVHAV 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs., 2284552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New:

- 1: /EMC Celleria_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.psp.*
- 2: /EMC Celleria_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.psp.*
- 3: /EMC Celleria_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.psp.*
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- 5: /EMC Celleria_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.psp.*
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- 7: /EMC Celleria_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.psp.*
- 8: /EMC Celleria_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	90.6	234	6	US-10-953-349-26204
2	29	90.6	384	6	US-10-953-349-26203
3	29	90.6	415	6	US-10-953-349-26202
4	28	87.5	72	6	US-10-449-902-28647
5	28	87.5	155	6	US-10-449-902-38148
6	28	87.5	281	6	US-10-953-349-30764
7	28	87.5	323	6	US-10-953-349-362
8	28	87.5	365	6	US-10-953-349-361
9	28	87.5	401	6	US-10-953-349-360
10	28	87.5	413	6	US-10-449-902-41714
11	28	87.5	547	6	US-10-449-902-54651
12	28	87.5	615	6	US-10-449-902-41977
13	28	87.5	704	6	US-10-449-902-53328
14	28	87.5	1507	6	US-10-449-902-52930
15	27	84.4	85	6	US-10-449-902-50855
16	27	84.4	96	6	US-10-953-349-39938
17	27	84.4	98	6	US-10-953-349-39937
18	27	84.4	184	6	US-10-449-902-49063
19	27	84.4	387	6	US-10-449-902-45662
20	27	84.4	651	7	US-11-289-102-230
21	27	84.4	701	6	US-10-449-902-44370
22	26	81.2	170	6	US-10-953-349-8501
23	26	81.2	171	6	US-10-953-349-8500
24	26	81.2	172	6	US-10-953-349-8499
25	26	81.2	226	6	US-10-953-349-33173

26	81.2	254	6	US-10-953-349-33172	Sequence 33172, A
27	81.2	302	6	US-10-953-349-34847	Sequence 34847, A
28	81.2	319	6	US-10-953-349-8390	Sequence 8390, Ap
29	81.2	334	6	US-10-953-349-38055	Sequence 38055, A
30	81.2	336	6	US-10-953-349-8389	Sequence 8389, Ap
31	81.2	344	6	US-10-953-349-38054	Sequence 38054, A
32	81.2	344	6	US-10-449-902-53361	Sequence 53361, A
33	81.2	345	6	US-10-953-349-8388	Sequence 8388, Ap
34	81.2	350	6	US-10-449-902-32227	Sequence 32227, A
35	81.2	350	6	US-10-449-902-46552	Sequence 46552, A
36	81.2	351	6	US-10-449-902-32734	Sequence 32734, A
37	81.2	351	6	US-10-449-902-52691	Sequence 52691, A
38	81.2	368	6	US-10-953-349-38053	Sequence 38053, A
39	81.2	419	6	US-10-449-902-40819	Sequence 40819, A
40	81.2	446	6	US-10-953-349-34846	Sequence 34846, A
41	81.2	476	6	US-10-953-349-32591	Sequence 32591, A
42	81.2	497	6	US-10-953-349-34845	Sequence 34845, A
43	81.2	504	6	US-10-471-571A-4106	Sequence 4106, Ap
44	81.2	522	6	US-10-953-349-32590	Sequence 32590, A
45	81.2	525	6	US-10-953-349-32293	Sequence 32293, A

ALIGNMENTS

RESULT 1

US-10-953-349-26204
; Sequence 26204, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26204
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26204

Query Match 90.6%; Score 29; DB 6; Length 234;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6
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DB 85 HALHAV 90

RESULT 2

US-10-953-349-26203
; Sequence 26203, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26203
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26203

Query Match 90.6%; Score 29; DB 6; Length 384;

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; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38148
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38148

Query Match      87.5%; Score 28; DB 6; Length 155;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAVHAV 6
Db 94 HAVHV 99

RESULT 6
US-10-953-349-30764
; Sequence 30764, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30764
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30764

Query Match      87.5%; Score 28; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHA 5
Db 174 HAVHA 178

RESULT 7
US-10-953-349-362
; Sequence 362, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 362

Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAVHAV 6
Db 235 HALHAV 240

RESULT 3
US-10-953-349-26202
; Sequence 26202, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26202
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-26202

Query Match      90.6%; Score 29; DB 6; Length 415;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HAVHAV 6
Db 266 HALHAV 271

RESULT 4
US-10-449-902-28647
; Sequence 28647, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28647
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-28647

Query Match      87.5%; Score 28; DB 6; Length 72;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 HAVHAV 6
Db 39 HTHAV 44

RESULT 5
US-10-449-902-38148
; Sequence 38148, Application US/10449902
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 23, 2006, 20:49:15 ; Search time 51 Seconds
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Title: US-10-648-854-10

Perfect score: 32

Sequence: 1 HAVHAV 6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	32	100.0	107	2	US-09-270-767-37862
3	32	100.0	107	2	US-09-270-767-53079
4	32	100.0	566	2	US-09-252-991A-17799
5	32	100.0	615	2	US-09-939-853A-16
6	32	100.0	623	2	US-09-949-016-7142
7	32	100.0	1422	2	US-08-469-260A-81
8	32	100.0	1422	2	US-08-467-344A-81
9	32	100.0	1422	2	US-08-488-446-81
10	32	100.0	1422	2	US-08-424-550B-81
11	31	96.9	465	2	US-09-270-767-35705
12	31	96.9	465	2	US-09-270-767-50922
13	29	90.6	252	2	US-09-252-991A-28437
14	29	90.6	268	2	US-09-818-780-17
15	29	90.6	268	2	US-09-818-780-94
16	29	90.6	268	2	US-09-716-964B-156
17	29	90.6	447	2	US-09-540-236-3079
18	29	90.6	1051	2	US-09-252-991A-19145
19	28	87.5	19	1	US-08-505-377-4
20	28	87.5	19	2	US-08-798-269-4
21	28	87.5	19	2	US-09-055-210-4
22	28	87.5	222	2	US-09-252-991A-18423
23	28	87.5	248	2	US-09-502-540-16714
24	28	87.5	282	2	US-09-252-991A-31742
25	28	87.5	286	2	US-09-252-991A-29952
26	28	87.5	303	2	US-09-252-991A-19613

27	28	87.5	372	1	US-08-202-056-5	Sequence 5, Appli
28	28	87.5	372	1	US-08-076-093A-6	Sequence 6, Appli
29	28	87.5	372	1	US-08-701-265-6	Sequence 6, Appli
30	28	87.5	372	1	US-08-284-586-6	Sequence 6, Appli
31	28	87.5	372	1	US-08-805-478-6	Sequence 6, Appli
32	28	87.5	372	1	US-08-802-627A-6	Sequence 6, Appli
33	28	87.5	372	1	US-08-801-238-6	Sequence 6, Appli
34	28	87.5	372	1	US-08-801-228-6	Sequence 6, Appli
35	28	87.5	372	2	US-09-104-296-6	Sequence 6, Appli
36	28	87.5	372	2	US-08-982-493-8	Sequence 8, Appli
37	28	87.5	372	2	US-09-170-496B-66	Sequence 66, Appli
38	28	87.5	372	2	US-09-170-496D-200	Sequence 200, App
39	28	87.5	374	2	US-08-982-493-6	Sequence 6, Appli
40	28	87.5	378	2	US-09-949-016-10255	Sequence 10255, A
41	28	87.5	433	2	US-09-252-991A-21851	Sequence 21851, A
42	28	87.5	447	2	US-09-252-991A-32122	Sequence 32122, A
43	28	87.5	451	2	US-09-412-102-8	Sequence 8, Appli
44	28	87.5	451	2	US-09-217-787-8	Sequence 8, Appli
45	28	87.5	511	2	US-09-252-991A-31311	Sequence 31311, A

ALIGNMENTS

RESULT 1
US-08-939-853A-10
; Sequence 10, Application US/08939853A
; Patent No. 6203788
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING
; TITLE OF INVENTION: CELL ADHESION
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,853A
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 32,391
; REFERENCE/DOCKET NUMBER: 100086.402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-939-853A-10

Query Match 100.0%; Score 32; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAVHAV 6

Db 1 HAVHAV 6

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RESULT 2
US-09-270-767-37862
; Sequence 37862, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37862
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37862

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Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HAVHAV 6
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Db      81 HAVHAV 86

RESULT 3
US-09-270-767-53079
; Sequence 53079, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53079
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-53079

Query Match      100.0%; Score 32; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HAVHAV 6
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Db      81 HAVHAV 86

RESULT 4
US-09-252-991A-17799
; Sequence 17799, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17799
; LENGTH: 566
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17799

Query Match      100.0%; Score 32; DB 2; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HAVHAV 6
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Db      173 HAVHAV 178

RESULT 5
US-09-939-853A-16
; Sequence 16, Application US/09939853A
; Patent No. 6989232
; GENERAL INFORMATION:
; APPLICANT: Burgess et al.
; TITLE OF INVENTION: No. 6989232el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-099
; CURRENT APPLICATION NUMBER: US/09/939,853A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/228,191
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/267,300
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/269,961
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/277,337
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-853A-16

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HAVHAV 6
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Db      56 HAVHAV 61

RESULT 6
US-09-949-016-7142
; Sequence 7142, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7142
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7142
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